

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q6MG48	PRC2A_RAT	Rattus norvegicus	Protein PRC2A	23.439218	NaN	S18;S19;S30;S146;S166;S204;S342;S350;S363;S378;S381;S455;T609;S760;S762;S765;T808;S809;S936;T1000;S1007;T1086;S1088;S1092;S1095;T1097;S1109;S1113;S1123;S1150;S1222;S1307;S1311;T1324;S1326;S1329;T1348;T1354;S1385;S1387;T1406;S1761;S2040;S2086;S2117	38843836	MSDRSGPTAKGDKGKYSLLNLFDTYKGSLEIQKPAVAPRHGLQSLGKVAIARRMPPANLPSLKAENKGNPDNVSLVPKDGWASKQEQSDPKSSDASTAQPPESQPLPASQTPASNQPKRPPTAPENTPSVPSGVKSWAQASVTHGAHGDGGRASSLLSRFSREFFPTLQAAGDQDKAAKERESAEQSSGPGPSLRPQNSTTWRDGGGRGPDELEGPDSKLHGHGDPGRGLQPSGPPQFPYRGMMPPFMYPPYLPFPYGPQGPYRYPTDGPFRFPRVAGPRGSGPPMRLVEPVGRPSILKEDNLKEFDQLDQENDDGWAGAHEEVDYTEKLFKFSDEEDGRDSDEEGAEGHKDSQSAAGEEPETDGGKGTSPGSELPPPKTAWTENSRRPSETEPAAPPKPPPPPPHRRGVPVGNWGP GDYVDRGGPPCKPPAPEDEDEAWRQRRKQSSSEISLAVERARRRRREEEER RMQEERRAACAEKLRLEKDFGAPDKRLKAEPAPVTPPAPALPPVVKETPTPALPPTPTPEKDPPEEPAHA PPVQSAPTQAGPPAPTVPVSGGTASS TSSGSFEASPAEPQLPSKEGPEPPEE VPAPTPPAPKVEPKGDGVPTROPP SQGLGYPKYQKSLPPRFQRQQEQQL LKQQQQQQWQQQQQQGTAPPAPV PPSPPQPVTLGAVPAPAPPPPKAL YPGALGRPPMPPMNFDRWMMIP PYVDPRLQGRPLDFYPPGVHPSGL VPRESDSGSSSEPFERHAPLLR ERGTPPVDPKLAWVGDVFTTPTDP RPLTSPLRQAADDEEKSRLRSETPPV PPPPYLANYPGFENGTGPPISRFP LEESAPPGRPLPWPPGNDEAAKMQ APPPKKEPKKEPAQLSGEAGRKPA RGVGGGGQGGPPRRENRTETRWG PRPGSCRRGIPPEDPGVPPRRAGPIK KPPPPVKADELPPKSLEPGDETPKAP KPDALKTAKGKVPKETPAGGNLSP APRLRDYSYERVGTSCRRGRGE YFARGRFRGTGGRRGRARSREFR SYREFRGDDGGGGSGGTNHPSAP RGRTASETRSEGSEYEIIPKRRRQRG SETGSETHESDLAPSDKEAPPPKEG VLAQVPLAPPQGPSPAPARFSTA RGGRVFTPRGVPSRRRGGGRPPV CSGWSPPAKSLVPKPPPTGPLPNK EPLKEKLISGLSPMSRAGNMGVGM EDGERPRRRRHGRAQQDKPPFR RLKQDRENAARGTDGKPPPLTPAS TPAPTETLATVAAPPPRRRTAAKSPD LSNQNSDQANEWETASESSDFAS ERRGDKETPPAALITSKAVGTPGGNS GGAGPGISTMSRGDLSQRAKDLSKR SFSSQRPMDRONRRRPGAGGKTGG GSSGGGGAGPGGRTGPGRGDKRS WPSPKNRSRPPPEERPPGLPLPPPPS SSAVFRLDQVIHSNPAGIQQALAOLS SRQGNVTAAGGHPRPKPPQAPQG SSPRPPTHYDPPRASNAISSDPHFEE PGPVVRGVGTPRDSAGVNPFPKR RERPPRKPELLQEETVPASHSSGFL GSKPEVPGQEESSRDSGTEALTPHI WNRLHTATSRKSYQPGSIEPWMEPL SPFEDVAGTEMSQSDSGVDLSGGSQ VSSGPCSQRSSPDGGLKGSAGPPR RPPASHEGERKELPREQPLPPGPIG TERSQRTDRGPEGPLRPAHRAGSQ VEFGTTNKSDLDLCLVVDLTKGEKE LAASATEAVVSRDWELLPSASASAE PQAQSLGSGQCGPEPSPSGQRLYPE VFYGSPPNSQVSGGAPIDSQHLHPS SGGFRPGTSPVHQYRSQPLYLPPGP APPSALLSGVALKGQFLDFALQATE LGKLPAGGVLYPPPSFLYSAAFPCSP LPDPPLLQVRQDLSPSPDFYSTPLQP GGSQGFPSGAPAQMLLPVVDSQL	True	False	2.324	4.298	0.888	0.613	0.391	0.999	0.709

